

BLASTP ALIGNMENT OF SEQ ID NO: 5 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 5)  
Subject: -gi|5213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
Length = 243

Score = 158 (60.7 bits), Expect = 1.3e-08, P = 1.3e-08

Identities = 42/136 (30%), Positives = 67/136 (49%)

Query: 670 RVAFSAARTSNLAPGTLDQPIVFDLNLNNLGETFDLQLGRFNCPVNGTYVFIFHMLKLA 728  
R AFS T P + PI F + N +D G+F+C + G Y F +H+  
Sbjct: 111 RSAFSVGLETYVTVP--NMPIRFTKIFYNQQNHYDGSTGKPHCNIPGLYYFAYHITVYM 167

Query: 729 VNVPLYVNLMKNEEVILVSAYANDGAPDHETASNHAIIQLFQGDQIWLRLH----RGAIIYG 784  
+V V+L K ++ ++ Y + + AS +L L GDIQ+WL++ R +Y  
Sbjct: 168 KDVK--VSLFKKDKAAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYCEGERNGLYA 225

Query: 785 SSWKYSTFSGYLLYQD 800  
+ STF+G+LLY D  
Sbjct: 226 DNDNDSTFTGFLLYHD 241

FIG. 1

BLASTP ALIGNMENT OF SEQ ID NO: 5 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 5)  
Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human

adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 156 (60.0 bits), Expect = 4.3e-09, P = 4.3e-09

Identities = 41/136 (30%), Positives = 67/136 (49%)

Query: 670 RVAFSAAR-TSNNLAPGTLLDQPIVFDLILNNLGETFDLQLGRFNCPVNGTYVFLFHMILKA 728  
R AFS T P + P F + N +D G+F+C + G Y F +H+

Sbjct: 112 RSAFSVGLETYYTIP---NMPPERFTKIFYNQQNHYDGSTGKPHCNIPGLYYFAYHITYM 168

Query: 729 VNVPLIYVNLMKNEEVLVSAVYANDGAPDHETASNHALLQLFQGDQIWLRLH----RGAIYG 784  
+V V+L K ++ Y ++ AS +L L GQD+WL++ R +Y

Sbjct: 169 KDVK--VSLFKKKDKAAMLFTYDQYQENNYDQASGSVLLHLEVGDQWLQVYCEGERNGLYA 226

Query: 785 SSWKYSTFSGYLLYQD 800

+ STF+G+LLY D

Sbjct: 227 DNDNDSTFTGFLLYHD 242

FIG. 2

BLASTP ALIGNMENT OF SEQ ID NO: 15 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 15)  
Subject: gi|5213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
Length = 243

Score = 147 (56.8 bits), Expect = 2.6e-07, P = 2.6e-07

Identities = 40/136 (29%), Positives = 65/136 (47%)

Query: 580 RVAFSAAR-TISNLAPGTLIDQPYGVDLLNNLNGETFDLQLGRFNCPVNGTYYVFLFHMLKLA 638  
R AFS T P + P + N +D G+F+C + G Y F +H+  
Sbjct: 111 RSAFSVGLETYVTVP--NMPIRFTKIFYNQQNHYDGSTGKPHCNIPGLYXFAYHITYM 167

Query: 639 VNVPLYVNLMKNEEVILVSAYANDGAPDHETASNHAIIQLFQGDQIWLRLH----RGAIYG 694  
+V V+L K ++ ++ Y + + AS +L L GDQ+WL++ R +Y  
Sbjct: 168 KDVK--VSLFKKDKAAMLFTYDQYQENNVDQASGSVLLHLEVGQDWLQVYCEGERNGLYA 225

Query: 695 SSWKYSTFSGYLLYQD 710  
+ STF+G+LLY D  
Sbjct: 226 DNDNDSTFTGFLLYHD 241

FIG. 3

BLASTP ALIGNMENT OF SEQ ID NO: 15 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 15)  
Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 151 (58.2 bits), Expect = 1.5e-08, P = 1.5e-08

Identities = 40/136 (29%), Positives = 66/136 (48%)

Query: 580 RVAFSAA-RTSNLAPGTLDQPYGVDLNNLNLGETFDLQLGRFNCPVNGTYVFIFHMLKLA 638  
R AFS T P + P + N +D G+F+C + G Y F +H+  
Sbjct: 112 RSAFSVGLETYYTIP--NMPPERFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAYHITVYM 168

Query: 639 VNVPLYNNLMKNEEVLVSAVANDGAPDHETASNHAILQLFQGDDQIWLRLH---RGAIYG 694  
+V V+L K ++ Y +++ AS +L L GDD+WL+++ R +Y  
Sbjct: 169 KDVK- -VSLFKKDKAMLFYDQYQENNYDQASGSVLLHLEVGDQVWLQVYGEGERNGLYA 226

Query: 695 SSWKYSTFSGYLLYQD 710  
+ STF+G+LLY D  
Sbjct: 227 DNDNDSTFTGFLLYHD 242

FIG. 4

**BLASTP ALIGNMENT OF SEQ ID NO: 28 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)**

Query:	Adiponectin-Like Polypeptide (SEQ ID NO: 28)	
Subject:	gi 15213856 AF404407_1 (AF404407) adiponectin [Macaca mulatta]	(SEQ ID NO: 402)
	Length = 243	
Score =	351 (128.6 bits), Expect = 7.7e-31, P = 7.7e-31	
Identities =	84/225 (37%), Positives = 124/225 (55%)	
Query:	525 GPPGFPGIGKPGVAG-LHGPPGKPGALGPQQGPGLPGPPGPPGPPGPPAVMPPPTPPPQQGE 583	
Sbjct:	GP + K G + G PG PG G G+ G G PG G G P ++ P +G	
Query:	584 YLPDMG-LGIDGVKPKPHAYGAKGKGNGP--AYEM-PAFTAELTAPFPVPGAPVKFNKL 638	
Sbjct:	D G G+ G + P + +G+ G P AY AF+ L P++F K+	
Query:	639 LYNGRQNYNPQTGIFTCEVPGVYYFAYHWHCKGGNIVVALFKNNNEPVMYTYDEYKKGFLD 698	
Sbjct:	YN + +Y+ TG F C +PG+YYFAYH+ +V V+LFK ++ +++TYD+Y++ +D	
Query:	135 FYNQQNHYDGSTGKFCNCIPGLYYFAYHITVYMKDVKVSLFKDKAMLFTYDQYQENNVD 134	
Sbjct:	FYNQQNHYDGSTGKFCNCIPGLYYFAYHITVYMKDVKVSLFKDKAMLFTYDQYQENNVD	
Query:	699 QASGSAVLRLRPDRVFLQMPSE-QAAGLYAGQYVHSSFSGYLLY 742	
Sbjct:	QASGS +L L GD+V+LQ+ E + GLYA S+F+G+LLY	
	195 QASGSVLLLHLEVGDDQVWLQVYGEGERNGLYADNDNDSTFTGFLLLY 239	

**FIG. 5**

BLASTP ALIGNMENT OF SEQ ID NO: 28 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 28)  
Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 363 (132.8 bits), Expect = 6.7e-33, P = 6.7e-33

Identities = 87/236 (36%), Positives = 129/236 (54%)

Query: 514 IPGPKGEPLGPGLPFPGLKPGVAG-LHGPPGKPGALGPQGQPGQPLGPGLPQGPPGPPGPPA 572  
+PG E + GP + K G + G PG PG G G+ G PG G G P  
Sbjct: 13 LPGHDQETTIQGPVVLPLPKGACTGWMAGIPGHPCNGAPGRDGRDGTPEKGEKGDPG 72

Query: 573 VMPPTPPQQEYLPDMG-LGIDGVKPPHAYGAKKGKNGGP--AYEM-PAFTAELTAPFP 627  
++ P +G D+G G+ G + P + +G+ G P AY AF+ L +  
Sbjct: 73 LIGP---KG---DIGETGVPGAAEGRPGFPGIQGRKGEPEGAYVYRSAFEVGLETYYT 124

Query: 628 PVGAPVKFNKLLYNGRQNYNPQTGIFTCEVPGVYYFAVHVKGGNVWVALLFKNNNEPVMY 687  
P +F K+ YN + +Y+ TG F C +PG+YYFAVH+ +V V+LFK + + +  
Sbjct: 125 IPNMPERFTKIFYNQQNHYDGSTGKFHCNCNIPGLYYFAVHITVYMKDVVKVSLFKKDAMLF 184

Query: 688 TYDEYKKGFLDQASGSAVLLRPDRVFLQMPSE-QAAGLYAGQYVHSSFSGYYY 742  
TYD+Y++ DQASGS +L L GD+V+LQ+ E + GLYA S+F+G+LLY  
Sbjct: 185 TYDQYQENNYYDQASGSVLLHLEYGDQVWLQVYGEGERNGLYADNDNDSTFTGFLY 240

FIG. 6

## BLASTP ALIGNMENT OF SEQ ID NO: 160 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 160)  
 Subject: gi|5213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 410 (149.4 bits), Expect = 5.3e-38, P = 5.3e-38

Identities = 92/228 (40%), Positives = 133/228 (58%)

Query: 53 GPHGRIGLPLGRDGRDGRKGEKGEKGKTAGLRLGKTPGLGLAGEKGKDQGETGKKGPIGPGEEK 112  
 Sbjct: 23 GPGVLLPLPKGACTGWMAGIPGHPGHNGVPGRDGRDGTGPKGEKGDPGL--IGPKGDT 79

Query: 113 GEVGPPIGPGPKGDKDRGEQGDGPLPGVCRCGSIVLKSAFSVGITTSYPEERLPLIFENKVLF 172  
 Sbjct: 80 GETGVTGAEGPRGFPGIQRKGEPGE ---GAYVYRSAFSVGLEYTVTVPNNMPIRFTKIFY 136

Query: 173 NEGEHYNPATGKFICAFPGIYFSYDITLANKHLAIGLVHNGQYRIKTFDANTGNH-DVA 231  
 Sbjct: 137 NQQNHYDSTGKPFHCNIPGLYYYFAYHITVYMKDVKVSLSFKKDKAAMLFTYDQYQENNVDQA 196

Query: 232 SGSTVILQPEDEVWLEIFFT-DQNLFSDPGWADSLFSGFLLYVDTD 278  
 Sbjct: 197 SGSVLLHLEVGDQWVQVYGEGERNGLYADND-NDSTFTGFLLYHDTN 243

BLASTP ALIGNMENT OF SEQ ID NO: 160 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query:	Adiponectin-Like Polypeptide (SEQ ID NO: 160)
Subject:	AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)
Length:	244
Score:	411 (149.7 bits), Expect = 7.3e-39, P = 7.3e-39
Identities:	94/238 (39%), Positives = 134/238 (56%)
Query:	PGPPGANGSPGPAPHGRIGLPGRDGRKGEKGEKGTAGLRGKTGPLGLAGAKGDQGETGK 102
Subject:	PG GP + LP G G G G+ G G GEKG++G+ G PGHQETTIQGPGVLLPLPKACTGWMAGIPGHGPNGAPGRDGRDGTGPKGEKGDGPL 73
Query:	KGPIGPEGEKGEVGPIGPPGPKDRGEQGDPGLPGVCRCGSIVLKSAFFSVGITTSYPEER 162
Subject:	IGP+G+ GE G GP+G G OG G PG G+ V +SAFSVG+ T Y ---IGPKGDIGETGVPGAEGGPRGFPGIQRKGEPE-- -GAYVYRSAFSGVLETTYPTPN 127
Query:	LPIIFNKVLFNEGEHYNPATGKFICAFPGIYYFSYDITLANKHLAIGLVHNGQYRIKTFD 222
Subject:	+P F K+ +N+ HY+ +TGKF C PG+YYF+Y IT+ K+ + L + + T+D MPERFTKIFYNQONHYDGSTGKFHNCNIPGLYYPAYHITVYMKDVKVSLLFKDKKAMLFYTD 187
Query:	A-NTGNHVDVASGSTVYIQLQPEDDEVWLEIIFTT-DQNGLFSDPGWADSLFSGFLLYVDTD 278
Subject:	N+D ASGS +++L+ D+VWL+++ ++NGL++D DS F+GFLLY DT+ QYQENNNYDQASGSVLLHLEVGQVWLNQVYGEGERNGLYADND-NDSTFTGFLYHDTN 244

## BLASTP ALIGNMENT OF SEQ ID NO: 186 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 186)  
 Subject: gi|15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 472 (171.2 bits), Expect = 1.4e-44, P = 1.4e-44

Identities = 104/204 (50%), Positives = 130/204 (63%)

Query: 86 GI|KGDQGSRGSPGKHGPGLAGPMGEKG|LRLGETGPQQGKGNKG|VGP|GPRGN|GPL 145  
 Sbjct: 41 G|P|GHPG|HNGVPG|GRDGT|PGEK|GEKGD|PGL|GP--K|GDT|GET|GVT|GAEG|PRGF|PG|Q 97

Query: 146 GPTGLP|PMGP|IGKPG-PKG-EAGPTGPQDMP|KF|DKI|LYNE|FF|NH|Y|DTAAGK|FT|CH|IAGV 203  
 Sbjct: 98 GRK|GEP|GEG|AYVY|RS|A|F|SV|G|L|E|TY|V|T|V|P-N|MP|IR|FT|K|I|FY|N|Q|N|H|Y|D|G|S|T|G|K|F|H|C|N|I|P|G|L 156

Query: 204 YYFTYH|ITV|FSRNV|QVSLV|KNGV|KILH|T|KDAY|MS|SE-DQASGG|IVL|QL|KL|G|DEV|WL|QV|TG 262  
 Sbjct: 157 YYF|YH|ITV|++V|VSL|K|+L|T|D|Y|+DQASG|++L|L|+|GD|+V|WL|QV|G 216

Query: 263 -GERFNGLFADED|DDTT|FTG|FLLF 285  
 Sbjct: 217 EGER-NGLYADNDND|S|FTG|FLLY 239

FIG. 9

**BLASTP ALIGNMENT OF SEQ ID NO: 186 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)**

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 186)  
 Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
 adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
 Length = 244

Score = 458 (166.3 bits), Expect = 7.6e-44, P = 7.6e-44

Identities = 102/204 (50%), Positives = 129/204 (63%)

Query: 86 GIKGDQGSRGSPGKGPKGLAGPMGEKGLRGETGPQQGKGNKGDVGPTGPEGPRGNIGPL 145  
 GI G G G+PG+ G G GEKG G GP KG+ G+ G EGPRG G  
 Sbjct: 42 GIPGHPGHNGAPGRDGRDGPGLIGP---KGDIGETGVPGAEGRGPRGFPGIQ 98

Query: 146 GPTGLPGPMGPIGKPG-PKG-EAGPTGPQDMPIKFDKILYNEBFNHYDTAAGKFTCHIAGV 203  
 G G PG + + G E T P +MP +F KI YN+ NHYD + GK F C+I G+  
 Sbjct: 99 GRKGEPEGEGAYVYRSAFSVGLEYTYTIP-NMPPERFTKIFYNQQNHYDGSTGKFHNCNIPGL 157

Query: 204 YYFTYHITVFSRNVQVSLVKNGVKILHTKDAYMSSE-DQASGGIVLQLKLGDEVWLQVTG 262  
 YYF YHITV+ ++V+VSL K +L T D Y + DQASG + +L L+ +GD+VWLQV G  
 Sbjct: 158 YYFAYHITVYMKDVVKVSLFKKDAMLFTYDQYQENNYYDQASGSVLLHLEVGDQVWLQVYVG 217

Query: 263 -GERFNGLFADEDDDTTFTGPLL 285  
 GER NGL+AD D+D+TFTGFLL+  
 Sbjct: 218 EGER-NGLYADNDNDSTFTGFLLY 240

## BLASTP ALIGNMENT OF SEQ ID NO: 215 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 215)  
 Subject: gi|15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 208 (78.3 bits), Expect = 1.4e-16, P = 1.4e-16

Identities = 57/178 (32%), Positives = 86/178 (48%)

Query: 104 GLAGPMGEKGGLRGETGPQQKGKGNKGDVGPPTGPEGPGRGNIGPLCPTGLPGPMGPIGKPGPK 163  
 Subject: 41 GIPGHPGHNNGVPGGRDGTGPKDGLIGPKGDTGETGVTGAEGPGRGFPGIQGRK 100

Query: 164 GEAGPTGQGEPGVR-GIRGWKGDRGEKGKIGETLVLPKSAFTVGLTVLSKFPSDDVPIK 222  
 Subject: 101 GEPGEGAYVYRSAFVGLEYTTVPNMPIRFTKIFYNQQNHYD-GST--GKFHCNIPGLY 157

Query: 223 FDKIHITVFSRNVQVSLVKNGVKILHTRDAYSSE-DQASGSIVLQLKLGDEMWCVIH 279  
 Subject: 158 YFAYHITVYMKDVKKVSLFKKDVKMLFTYDQYQENNVIDQASGSVLLHLEVGDQVWLQVY 215

FIG. 11

BLASTP ALIGNMENT OF SEQ ID NO: 215 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

FIG. 12

## BLASTP ALIGNMENT OF SEQ ID NO: 241 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 241)  
 Subject: gi|5213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 476 (172.6 bits), Expect = 5.4e-45, P = 5.4e-45

Identities = 101/202 (50%), Positives = 129/202 (63%)

Query: 131 GPTGPEGPRGNIGPLGPTGLPGPMGPPIGKPGPKGEAGPTGPQGEPGVQGIRGKGDRCGEK 190  
 Sbjct: 41 GIPGHPGHNNGVPGRDGTGPKDGLIGPKGDTGETGVTGAEGPGRGFPGIQGRK 100

Query: 191 GKIGETLVLVLPKSAFTVGLTVLSKFPSSDRPIKFDKILLYNEFNHYDTAAGKFTCHIAGYYY 250  
 Sbjct: 101 G+ GE + +SAF+VGL P+ PI+F KI YN+ NHYD + GKF C+I G+YY

Query: 251 FTYHITVFSRNVQVSIVKNGVKILHTKDAYMSSE-DOASGGIVLQLKLGDEVWLQVTG-G 308  
 Sbjct: 159 FAYHITVYMKDVVKVSLFKKDKAAMLFTYDQYQENNVDQASGSVLLHLEVGDQVWLQVYGEG 218

Query: 309 ERFNGLFADEDDDTTFTGFLLF 330  
 Sbjct: 219 ER-NGLYADDNDNSTFTGFLLY 239

**FIG. 13**

BLASTP ALIGNMENT OF SEQ ID NO: 241 WITH HUMAN ADIPONECTIN  
 AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 241)  
 Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
 adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
 Length = 244

Score = 473 (171.6 bits), Expect = 2.0e-45, P = 2.0e-45

Identities = 100/202 (49%), Positives = 128/202 (63%)

Query: 131 GPTGPEGPRGNITGPLGPTGLPGPMGPIGKPGPKGEAGPTGPGQGEAGPTGPGQGVQGIRGWKGDRGEK 190  
 G G G G G PG G G PG G G PG G G PG +G RG+ G +G K  
 Sbjct: 42 GIPGHPGHNNGAPGRDDGRGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRK 101

Query: 191 GKGETLVLPKSAFTVGLTVLSKFSSDRPIKFDKILLYNEFNHYDTAAGKFTCHIAGVYYY 250  
 G+ GE + +SAP+VGL P+ P +F KI YN+ NHYD + GKF C+I G+YY  
 Sbjct: 102 GEPGEGAYVYRASFVSGLETTYPTPNM--PERFTKIFYNQQNHYDGSTGKFHCNIPGLYY 159

Query: 251 FTYHITVFSRNVQVSLSVKNGVKILHTKDAYMSSE-DQASGGIVLQLKLGDEVWLQVTG-G 308  
 F YHITV+ ++V+VSL K +L T D Y + DQASG ++L L+GD+VWLQV G G  
 Sbjct: 160 FAYHITVYMKDVKVSLFKDKAMLFYDQYQENNYDQASGSVLLHLEVGDQWVLQVYGEQ 219

Query: 309 ERFNGLFADEDDDTTFTGFLFF 330  
 ER NGL+AD D+D+TFTGFLL+  
 Sbjct: 220 ER-NGLYADDNDNDSTFTGFLLY 240

FIG. 14

BLASTP ALIGNMENT OF SEQ ID NO: 272 WITH  
ADIPOSE TISSUE-SPECIFIC PROTEIN ADIPO Q (SEQ ID NO: 403)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 272)  
Subject: gi|4289336 AF269230\_1 (AF269230) adipose tissue-specific protein adipo Q  
[Bos taurus] (SEQ ID NO: 403) Length = 240

Score = 212 (79.7 bits), Expect = 1.0e-34, Sum P(2) = 1.0e-34

Identities = 41/78 (52%), Positives = 56/78 (71%)

Query: 227 HITVFSRNVQVSLLVKNGVKILHTKDAYMSSE-DQASSGGIVLQLKLQVTLQVGGGERFN 285  
HITV+ ++V+VSL K +L T D Y DQASG ++L L+GD+VWLQV GE N  
Sbjct: 158 HITVYMKDVKVSLFKDKAVLFTYDQYQEKNVDQASSGVLLHLEVGDQWVLQVYEGENHN 217

Query: 286 GLFADEDDDTTFTGFLLF 303  
G++AD +D+TFTGFLL+  
Sbjct: 218 GYYADNVNDSTFTGFLLY 235

FIG. 15a

BLASTP ALIGNMENT OF SEQ ID NO: 272 WITH  
ADIPOSE TISSUE-SPECIFIC PROTEIN ADIPO Q (SEQ ID NO: 403)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 272)  
Subject: gi|4289336 AF269230\_1 (AF269230) adipose tissue-specific protein adipo Q  
[Bos taurus] (SEQ ID NO: 403) Length = 240

Score = 183 (69.5 bits), Expect = 1.0e-34, Sum P(2) = 1.0e-34

Identities = 43/100 (43%), Positives = 56/100 (56%)

Query: 6 LLLAIEIICGNINSQD-----TCRQGHPGIPGPNPQHNGLPGRDGRDGAKGDKGDAAGEPG 59  
Subject: 9 LLLA+ G N +D C GIPG+PGHNG PGRDGRDG G+KG+ G+ G  
Sbjct: 9 LLLALP-SHGEDNMEDDPPLPKGACAGWMAGIPGHPGHNGTPGRDGRDGTPGEKGEKGDAAG 67

Query: 60 RPPGSPGKDGTSGEKGKGERGADGKVEAKGIKGDQGSRGSPGK 99  
Subject: 68 LLGPKGE- -TGDVGMTGAEGP- -RGFPPTPGRKGEPEGE 101

FIG. 15b

BLASTP ALIGNMENT OF SEQ ID NO: 272 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 272)  
 Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
 adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
 Length = 244

Score = 307 (113.1 bits), Expect = 7.6e-28, P = 7.6e-28

Identities = 84/200 (42%), Positives = 109/200 (54%)

Query: 131 GPTGPEGPRGNIGPLGPTGLPGMPGPIGKPGPKGEAGGPTGPGQGPGVQGIRGWKGDRGEK 190  
 G G G G G G G PG G G PG G G PG G G PG +G RG+ G +G K  
 Sbjct: 42 GIPGHPGHNGAPGRDGRDTPGEKGEKGDPLIGPKGDIGETGVPGAEGRGPRGFPGIQGRK 101

Query: 191 GKIGETLVLPKSAFTVGLTVLSKFPSS-DRPIK-----FD-----KIH-----227  
 G+ GE + +SAF+VGL P+ +R K +D K H  
 Sbjct: 102 GEPGEGAYVYRSAFSGVLEYYTIPNMPPERFTKIFYNQQNHYDGSTGKFHCNIPGLYYFA 161

Query: 228 -ITVFSRNVQVSLVKNGVKILLHTKDAYMSS-E-DQASGGIVLQLKLGDEVNLQVTG-GER 283  
 ITV+ +V+VSL K +L T D Y + DQASG ++L L+ +GD+VNLQV G GER

Sbjct: 162 YHITVYMKDVVKVSLFKDKAMLLFTYDQYQENNYDQASGSVLLHLEVGDQWNLQVYGBGER 221

Query: 284 FNGLFADEDDDTTFTGFLLF 303  
 NGL+AD D+D+TFTGFLL+  
 Sbjct: 222 -NGLYADNDNDSTFTGFLLY 240

## BLASTP ALIGNMENT OF SEQ ID NO: 302 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 302)  
 Subject: gi|5213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 330 (121.2 bits), Expect = 1.6e-29, P = 1.6e-29

Identities = 82/220 (37%), Positives = 116/220 (52%)

Query: 124 PSTAATPDRGLMOSLPTFIQGPKEAGRPGKAGPRGPPGEPGPMPGMGPGEKGEPEGRQG 183  
 P A T G M + P G G GR G+ G G GE G PG +GP G+ GE G G  
 Sbjct: 31 PKGACT--GWMAGIPGH-PGHNNGVPGRDGRDGTGPGEKGEKDPGLIGPKGDTGETGYTG 86

Query: 184 LPGPPGAPGLNAA-GAISAATYSTGPKIAFYAGLKRQHEGYEV-LKFDDVVTNLGNHYDP 241  
 GP G PG+ G Y + AF GL+ + ++F + N NHYD  
 Sbjct: 87 AEGPRGFPGPQGRKGEPEGAYVY-RSAFSVGLETYVTVPNMPIRFTKIFYNQNMHYDG 144

Query: 242 TTGKFTCSIPGIYFFTYHVLMRGDDGTSWADLCKNNQVRASAIAQDADQNYDYASNSVV 301  
 +TGKF C+IPG+Y+F YH+ + D + L K ++ Q + N D AS SV+  
 Sbjct: 145 STGKFHCNIPGLYYFAHITVYMKD---VKVSLFKDKAMLFYDQYQENNVDQASGSVL 201

Query: 302 LHLEPGDEVYIKLDG-GKAHG-GNNNKYSTFSGFIIYAD 338  
 LHLE GD+V+++ G G+ +G +N+ STF+GF+Y D  
 Sbjct: 202 LHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLIYHD 241

**BLASTP ALIGNMENT OF SEQ ID NO: 302 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)**

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 302)  
 Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
 adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
 Length = 244

Score = 336 (123.3 bits), Expect = 5.8e-31, P = 5.8e-31

Identities = 83/220 (37%), Positives = 117/220 (53%)

Query: 124 PSTAATPDRGLMOSLPTFIQGPCKGEAGRPGKAGPRGPPGEPGPPGMPGPPGEKGEPEGRQG 183  
 P A T G M +P G G GR G+ G G GE G PG +GP G+ GE G G  
 Sbjct: 32 PKGACT--GWMAGIPTH-PGHNNGAPGRDGRDGTPLIGPKGDIGETGVPG 87

Query: 184 LPGPPGAPGLNAA-GAISAATYSTGPKLAFYAGLKRQHEGYEVL-KFDDVVTVNLGNHYDP 241  
 GP G PG+ G Y + AF GL+ + + +F + N NHYD  
 Sbjct: 88 AEGPRGFPGQGRKKGEPGEAYVY--RSAFSVGLETYTYTIPNMPPERFTKIFYNQNHYDG 145

Query: 242 TTGKFTCSIPGIYFFTYHVLMRGGDTSMWADLCKNNQVRASAIAQDADQNYDYASNSVV 301  
 +TGKF C+IPG+Y+F YH+ + D + L K ++ Q + NYD AS SV+  
 Sbjct: 146 STGKFHNCNIPGLYYFAHYITVYMKD---VIVVSLFKDKAMLFYDQYQENNNYDQASGSVL 202

Query: 302 LHLEPGDEVYIKLDG-GKAHG--GNNNKYSTSGFIIYAD 338  
 LHLE GD+V+++ G G+ +G +N+ STF+GF++Y D  
 Sbjct: 203 LHLEVGDQVWLQVYGEGERGLYADNDNDSTFTGFLLYHD 242

BLASTP ALIGNMENT OF SEQ ID NO: 323 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 323)  
 Subject: gi15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 330 (121.2 bits), Expect = 1.6e-29, B = 1.6e-29

Identities = 82/220 (37%), Positives = 116/220 (52%)

Query : 3.0 PSSTAATPDRGLMOSI,PTEFIGPKGEAGRPGKAGPRGPBDMGDDGEGEDCPOC 80

Query: 90 LPGPBPGAPGLNAA-GAISAATYSTGPKIAFYAGI.KROHEGCVEV-LKEFDVAVTNTGNTYD 117

Query : 14.8 TTGKETCSIPGIYEFTHYHVLMRGGDGTSMMWADIICKNNNOVBARASATIAQDADONVYDVA<sup>SN</sup>SNVY 207

Query: 208 LHLPEPSGDEWYIKLIDG-GKAHG--GNNNNKYSTESCGELIYD 244

Subject: 282 EHLIEYGDQWILQVYGEGERNGI.YADNNNTSTETGEL.YHD 241

FIG. 19

BLASTP ALIGNMENT OF SEQ ID NO: 323 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 323)  
Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 336 (123.3 bits), Expect = 5.8e-31, P = 5.8e-31

Identities = 83/220 (37%), Positives = 117/220 (53%)

Query: 30 PSTAAATPDRGLMQSLPTFIQGPKGAEGRPGKAGPRGPPGEPGPPGPPGEKGEPRGQ 89  
P A T G M +P G G GR G+ G G GE G PG +GP G+ GE G G  
Sbjct: 32 PKGACT--GWMAGIPIGH-PGHNNGAPGRDGRDGTGPKGEKGDPPGLIGPKGDIGETGVPG 87

Query: 90 LPGPPGAPGLNAA-GAISAATYSTGPKIAFYAGLKRQHEGYEVL-KFDDVVTVNLGNHYDP 147  
GP G PG+ G Y + AF GL+ + + +F + N NHYD  
Sbjct: 88 AEGPRGFPGIQRKGEPEGAYVY-RSAFSVGLLETYYTIPNMMPERFTKIFYNQONHYDG 145

Query: 148 TTGKFTCSIPGIYFFTYHVLMRGDGTSWADLCKNNDQVRASAIAQDADQNYDASNSVV 207  
+TGKF C+IPG+Y+F YH+ + D + L K ++ Q + NYD AS SV+  
Sbjct: 146 STGKFPHCNIPGLYYFAHYHITVYMKD---VKVSLFKDKAMLFYDQYQENNNYDQASGSVL 202

Query: 208 LHLEPGDEVYIKLDG-GKAHG--GNNNKYSTFSGFLIYAD 244  
LHLE GD+V+++ G G+ +G +N+ STF+GF++Y D  
Sbjct: 203 LHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLLYHD 242

FIG. 20

**BLASTP ALIGNMENT OF SEQ ID NO: 348 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)**

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 348)  
Subject: gi|15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
Length = 243

Score = 138 (53.6 bits), Expect = 1.9e-06, P = 1.9e-06

Identities = 69/220 (31%), Positives = 90/220 (40%)

Query: 296 PQQPGSTGIVIAETGQAGPPAGAGVSGR-GLPRLRGVDGQGTGSCTVPPGAEGFAGAGAPGYPKSPP 354  
Subject: 43 PGHPGHNGVPGRDGRDGTGPGEKGEKGDPGLI-GPKGDTGETGVTVGAEGPGRGFPGIQGRKG 101

Query: 355 VASPGAPVPSLVSFSAGL-TQKPFPSDGGVVLFNKKVVLVNDGDVYNPSTGVFTAPYDGRYL 413  
Subject: 102 EPGEGLAYVYRS-AFSGVGLETYVTVNMP--IRFTKIIFYNQQNHYDGSTGKFHNCNIPGLYY 158

Query: 414 ITATLTPERDAYVEAV-LSVSNAVASVAQLHTAGYRREFLEYHRPTGALHTCCGGPAGFHLLIV 472  
Subject: 159 FAYHIT---VYMKDVKVSLFKDKAMLFY---Y----DQYQENNIVDQASGS-----VLL 202

Query: 473 HIKAGDAVNNVVVTG-----GKLAHTDFDEMYSFGVFLY 507

Subject: 203 HLEVGDDQWVLQVYGEGERNGLYADNDND---STFTGFLLY 239

**FIG. 21**

**BLASTP ALIGNMENT OF SEQ ID NO: 348 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)**

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 348)  
 Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
 adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
 Length = 244

Score = 132 (51.5 bits), Expect = 1.7e-06, P = 1.7e-06

Identities = 75/243 (30%), Positives = 98/243 (40%)

Query: 269 PRPSGPATAEDPGRRPVLPQRPPEERPPQQPPGSTGVIAETGQAGPPAGAGVSGRGLPRGV 328  
 P P G T G +P P P G E G+ G P G+ G P+G  
 Sbjct: 30 PLPKGACTGWMAG---I PGHPGHNGAPGRDGRDGTGPKGEKGD P---GLIG---PKGD 79

Query: 329 DGQTGSCTVPGAAEGFAGAPGYPKSPPVAVSPGAPVPSLVSFSAGL-TQKPFPSDGGVVLFN 387  
 G+TG VPGAEQ G PG GA V +FS GL T P+ F  
 Sbjct: 80 IGETG---VPGAEGRGFPGQGRKGEKGDGTGPKGEKGD P---GLIG---PKGD 79

Query: 388 KVLVNDGDVNPSTGVFTAPYDGRYLITATLPERDAYVEAV-LSVSNASVAAQLHTAGYR 446  
 K+ N + Y+ STG F G Y +T Y++ V +S+ A L T  
 Sbjct: 134 KIFYNQNHYDGSTGKFHNCNIPGLYYFAYHIT----VYMKDVKVSFLFKKD KAMLFTYDQY 189

Query: 447 REFLEYHRPTGA--LHTCGGPGAFHLIVHLKAGDAVVVVTGGKLAHTDFDEMYSFSGV 504  
 +E Y + +G+ LH G + L V+ G+ G A D D STE+G  
 Sbjct: 190 QEN-NYDQASGSVLLHLEVGDQVW-LQVY --GEGER----NGLYADNDND---STFTGF 237

Query: 505 FLY 507  
 Sbjct: 238 LLY 240

BLASTP ALIGNMENT OF SEQ ID NO: 355 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 355)  
Subject: gi|5213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
Length = 243

Score = 199 (75.1 bits), Expect = 1.2e-15, P = 1.2e-15

Identities = 53/134 (39%), Positives = 68/134 (50%)

Query: 37 PRGPGPDGAPASVPPFP-----PGAKGEVRRGKAGLRRGPPGPPGPRGPPGPPGPPG 91  
P+G G A +P P PG G G+ G +G PG GP+G GE G G G  
Sbjct: 31 PKG-ACTGWMAGIPGHPGHNGVPGRDGRDGTGPKGDTGETGVTGAEG 89

Query: 92 PPG-PGPGGVA- -PAAG-YVPRIAFYAGLRRPHEGYEV-LRFDDVVTVGNAYEAASGKF 146  
P G PG G P G YV R AF GL + +RF + N N Y+ ++GKF  
Sbjct: 90 PRGFPGIQGRKGEPEGEGAYVYRSAFSVGLIETYVTPNMPIRFTKIFYNQONHYDGSTGKF 149

Query: 147 TCPMPGVYFFAYHV 160  
C +PG+Y+FAYH+  
Sbjct: 150 HCNIPGLYYFAYHI 163

FIG. 23

BLASTP ALIGNMENT OF SEQ ID NO: 355 WITH HUMAN ADIPONECTIN  
 AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 355)  
 Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
 adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
 Length = 244

Score = 204 (76.9 bits), Expect = 6.3e-17, P = 6.3e-17

Identities = 54/134 (40%), Positives = 69/134 (51%)

Query:	37	PRGPGPDGAPASVPPFP-----PGAKGEYGRRGKAGLRLGPPGPPGPPGEPGRGPPG	91	
	P+G	G A +P P	PG G G G+ G +G PG	GP+G GE G PG G
Sbjct:	32	PKG-ACTGWMAGIPGHPGHNGAPGRDGRDGTPEKGEKGDPGLI	GPKGDIGETGVPGAE	G 90
Query:	92	PPG-PGPGGVA - PAAG-YVPRIAFYAGLRRPHEGYEVL-RFDDVVTNVGNAYEAASGKF	146	
	P G PG G P G IV R AF GL	+ + RF + N N Y+ +GKF		
Sbjct:	91	PRGFPGIQGRKGEPGEGAYVYRSSAFSVGLETYYTIPNMPERFTKIFYNQQNHYDGSTGKF	150	
Query:	147	TCPMPGVYFFAYHV	160	
	C +PG+Y+FAYH+			
Sbjct:	151	HCNIPGLYYFAYHI	164	

## BLASTP ALIGNMENT OF SEQ ID NO: 378 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 378)  
 Subject: gi|15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 297 (109.6 bits), Expect = 5.0e-26, P = 5.0e-26

Identities = 80/215 (37%), Positives = 113/215 (52%)

Query: 37 PRGPGPDGAPASVPPFP-----PGAKGEVRRGKAIGLRLGPPGPPGPRGPPGEPGRPGPPG 91  
 Sbjct: P+G G A +P P PG G G+ G+G PG GP+G GE G G G

Query: 31 PKG-ACTGWMAGIPGHPGHNGVPGRDGRDGTGPKGDTGETGVTGAEG 89

Query: 92 PPG-PPGGVA- -PAAG-YVPRIAFYAGLRRPHEGYEV-LRFDDVVTNVGNAYEAASGKF 146  
 Sbjct: P G PG G P G YV R AF GL + +RF + N N Y+ +GKF

Query: 90 PRGFPQIGQGRKGEPGEGAYVRSAFSVGLLETYVTPNMPIRFTKIFYNQONHYDGSTGKF 149

Query: 147 TCPMPGVYFFAYHVLLMRGGDGTSMWADLMKNGQVRASAIQDADQNYDYASNSVILHLDV 206  
 Sbjct: C +PG+Y+FAZH+ + D + L K + Q + N D AS SV+LHL+V

Query: 150 HCNIPGLYYFAYHITVYMKD---VKVSLFKKDAMLFTYDQYQENNNVDQASGSVLLHIEV 206

Query: 207 GDEVFIKLDG-GKVKHG--GNTNKKYSTFSGFIIYPD 238  
 Sbjct: GD+V+++ G G+ +G + + STF+GF+Y D

Query: 207 GDQVWLQVYGEGERNGLYADNDNDSTFTGFLLYHD 241

TELEGRAM - 120301 194450Z

BLASTP ALIGNMENT OF SEQ ID NO: 378 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 378)  
Subject: AAY85144 AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 310 (114.2 bits), Expect = 3.7e-28, P = 3.7e-28

Identities = 82/215 (38%), Positives = 115/215 (53%)

Query:	37	PRGGPPDGAPASVPPFP-----PGAKGEVGRGKAGLRRGPPGPRGPGEPRGPGG	91
	P+G	G A + P P G G G + G PG	GP+G
objct:	32	PKG-ACTGWMAGIPGHPGHNGAPGRDGRDGTGPGEKGDKDGLIPKGKDGETGVPGAE	90

Query:	92	PPG-PGPGGVA--PAAG-YVPIRAFYAGLRRPHEGYEVL-RFDVVTVNQHAYEAASGKF	146
	P G PG G P G YV R AF GL + + RF + N N.Y+ ++GKF		
Subject:	91	BRGFPGICGRXGEPEGAAYVRSAFASVGLETYTTIPNMPPERETKIFYNOONHYNGSTCKF	150

Query:	147	TCMPGIVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAIQDADQNYDYASNSVILHLDV	206
	C.+PG+Y+FAVH+ + D	+ L K + Q	+ NYD AS SV+LHL+V
Sbjct:	151	RCNIPGLYXYFAVHITVYMKD--VVKVSLFEKKDKAMITETVDOYOFNNVYDOASCSVVLHLY	207

Query:	207	GDEVFIKLGD-GKVKHG--GNTNKYSTFSGFIIYYPD	238
	GD+V+++	G+ +G + +	STF+GF++Y D
Subject:	208	GDNWMLQYGEGRNGTYADNDNDSTTGTGLYH	242